APPENDIX A

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the claims:

Please amend claims 1-20 and 22 as follows:

1. **(Amended)** A method for determining whether a subject has, or is at risk of developing, an abnormally low HDL level, comprising determining the identity of the allelic variant of a polymorphic region of the SR-BI gene of the subject and comparing the allelic variant of the subject with allelic variants associated with abnormally low HDL levels, to thereby determine whether the subject has an allelic variant of a polymorphic region of an SR-BI gene associated with an abnormally low HDL level.

2. **(Amended)** ~~A~~ The method of claim 1, wherein the polymorphic region is located in an exon.

3. **(Amended)** ~~A~~ The method of claim 2, wherein the exon is exon 8.

4. **(Amended)** ~~A~~ The method of claim 3, wherein the polymorphic region is a nucleotide polymorphism.

5. **(Amended)** ~~A~~ The method of claim 4, wherein the nucleotide polymorphism is located at position 41 of exon 8.

6. **(Amended)** ~~A~~ The method of claim 5, wherein nucleotide 41 of exon 8 of the SR-BI gene in a normal subject is a thymidine and the presence of a nucleotide other than a thymidine at position 41 of exon 8 in the SR-BI gene of a subject indicates that the subject has or is at risk of developing an abnormally low HDL level.

7. **(Amended)** ~~A~~ The method of claim 6, wherein the nucleotide other than a thymidine at position 41 of exon 8 is a cytidine.

8. **(Amended)** ~~A~~ The method of claim 1, wherein determining the identity of the allelic variant of a polymorphic region of an SR-BI gene comprises determining the identity of at least one nucleotide of the polymorphic region.

9. **(Amended)** ~~A~~ The method of claim 2, wherein determining the identity of the allelic variant of a polymorphic region comprises contacting a nucleic acid of the subject with at least one probe or primer which is capable of hybridizing to an SR-BI gene.

10. **(Amended)** ~~A~~ The method of claim 9, wherein the probe or primer is capable of specifically hybridizing to an allelic variant of the polymorphic region.

11. **(Amended)** ~~A~~ The method of claim 10, wherein the probe or primer is capable of specifically hybridizing to an allelic variant having a thymidine at position 41 of exon 8 of the SR-BI gene.

12. **(Amended)** ~~A~~ The method of claim 1, wherein the probe or primer has a nucleotide sequence from about 15 to about 30 nucleotides.

13. **(Amended)** ~~A~~ The method of claim 1, wherein the probe or primer is a single stranded nucleic acid.

14. **(Amended)** ~~A~~ The method of claim 1, wherein the probe or primer is labeled.

15. **(Amended)** ~~A~~ The method of claim 1, wherein determining the identity of the allelic variant of a polymorphic region is carried out by allele specific hybridization.

16. **(Amended)** ~~A~~ The method of claim 1, wherein determining the identity of the allelic variant of a polymorphic region is carried out by primer specific extension.

17. **(Amended)** ~~A~~ The method of claim 1, wherein determining the identity of the allelic variant of a polymorphic region is carried out by an oligonucleotide ligation assay.

18. **(Amended)** ~~A~~ The method of claim 1, wherein determining the identity of the allelic variant of a polymorphic region comprises performing a restriction enzyme site analysis.

19. **(Amended)** ~~A~~ The method of claim 18, wherein the restriction enzyme is a HaeIII enzyme.

20. **(Amended)** ~~A~~ The method of claim 1, wherein determining the identity of the allelic variant of a polymorphic region is carried out by single-stranded conformation polymorphism.

22. **(Amended)** ~~A~~ The method of claim 21, comprising determining the identity of the nucleotide at position 41 in exon 8 and/or nucleotide 54 in intron 5, wherein the presence of a cytidine at position 41 of exon 8 and/or the presence of a thymidine at position 54 of intron 5 indicates that the subject has or is at risk of developing an abnormally low HDL level.

APPENDIX B

1. A method for determining whether a subject has, or is at risk of developing, an abnormally low HDL level, comprising determining the identity of the allelic variant of a polymorphic region of the SR-BI gene of the subject and comparing the allelic variant of the subject with allelic variants associated with abnormally low HDL levels, to thereby determine whether the subject has an allelic variant of a polymorphic region of an SR-BI gene associated with an abnormally low HDL level.

2. The method of claim 1, wherein the polymorphic region is located in an exon.

3. The method of claim 2, wherein the exon is exon 8.

4. The method of claim 3, wherein the polymorphic region is a nucleotide polymorphism.

5. The method of claim 4, wherein the nucleotide polymorphism is located at position 41 of exon 8.

6. The method of claim 5, wherein nucleotide 41 of exon 8 of the SR-BI gene in a normal subject is a thymidine and the presence of a nucleotide other than a thymidine at position 41 of exon 8 in the SR-BI gene of a subject indicates that the subject has or is at risk of developing an abnormally low HDL level.

7. The method of claim 6, wherein the nucleotide other than a thymidine at position 41 of exon 8 is a cytidine.

8. The method of claim 1, wherein determining the identity of the allelic variant of a polymorphic region of an SR-BI gene comprises determining the identity of at least one nucleotide of the polymorphic region.

9. The method of claim 2, wherein determining the identity of the allelic variant of a polymorphic region comprises contacting a nucleic acid of the subject with at least one probe or primer which is capable of hybridizing to an SR-BI gene.

10. The method of claim 9, wherein the probe or primer is capable of specifically hybridizing to an allelic variant of the polymorphic region.

11. The method of claim 10, wherein the probe or primer is capable of specifically hybridizing to an allelic variant having a thymidine at position 41 of exon 8 of the SR-BI gene.

12. The method of claim 1, wherein the probe or primer has a nucleotide sequence from about 15 to about 30 nucleotides.

13. The method of claim 1, wherein the probe or primer is a single stranded nucleic acid.

14. The method of claim 1, wherein the probe or primer is labeled.

15. The method of claim 1, wherein determining the identity of the allelic variant of a polymorphic region is carried out by allele specific hybridization.

16. The method of claim 1, wherein determining the identity of the allelic variant of a polymorphic region is carried out by primer specific extension.

17. The method of claim 1, wherein determining the identity of the allelic variant of a polymorphic region is carried out by an oligonucleotide ligation assay.

18. The method of claim 1, wherein determining the identity of the allelic variant of a polymorphic region comprises performing a restriction enzyme site analysis.

19. The method of claim 18, wherein the restriction enzyme is a HaeIII enzyme.

20. The method of claim 1, wherein determining the identity of the allelic variant of a polymorphic region is carried out by single-stranded conformation polymorphism.

21. A method for determining whether a female subject has, or is at risk of developing, an abnormally low HDL level, comprising determining the identity of the allelic variant of a polymorphic region of the SR-BI gene of the subject and comparing the allelic variant of the subject with allelic variants associated with low HDL levels, to thereby determine whether the subject has or is at risk of developing an abnormally low HDL level.

22. The method of claim 21, comprising determining the identity of the nucleotide at position 41 in exon 8 and/or nucleotide 54 in intron 5, wherein the presence of a cytidine at position 41 of exon 8 and/or the presence of a thymidine at position 54 of intron 5 indicates that the subject has or is at risk of developing an abnormally low HDL level.

34. A method for predicting the effect of hormone replacement therapy on the HDL level in a female subject comprising identifying one or more allelic variants of the SR-B1 gene which are associated with abnormally low HDL levels in females, thereby predicting the effect of hormone replacement therapy on the HDL level in the subject.

35. The method of claim 34, wherein hormone replacement therapy results in an abnormally low HDL level.

36. The method of claim 34, wherein the allelic variants comprise a cytidine at position 41 of exon 8 and/or a thymidine at position 54 of intron 5.

37. The method of claim 34, wherein the female subject is postmenopausal.

38. A method of predicting the effect of hormone replacement therapy on a female subject, wherein the identification of allelic variants of the SR-B1 gene which are associated with abnormally low HDL levels in females results in a prediction that hormone replacement therapy will result in abnormally low HDL levels.